

10 30 50  
GTGAGATGGTGCCTTTCATGAATCCCCCAACAAGAGCCAAGCTCTCCATCTAGTGGACAG  
70 90 110  
GGAAGCTAGCAGCAAACCTTCCCTTCACTACGAACTTCATTGCTTGGCCCAAAAGAGAG  
130 150 170  
TTAATTCAATGTAGACATCTATGTAGGCAATTAACCTATTGATGTATAAACAGTTT  
190 210 230  
GCATTCATGGAGGGCAACTAAATACATTCTAGGACTTTATAAAGATCACTTTTATTTA  
250 270 290  
TGCACAGGTGGAACAAGATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTAT  
M D Y Q V S S P I Y D I N Y  
310 330 350  
TATACATCGGAGCCCTGCCCAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCT  
Y T S E P C P K I N V K Q I A A R L L P  
370 390 410  
CCGCTCTACTCACTGGTGTTCATCTTTGGTTTTGTGGCAACATGCTGGTCATCCTCATC  
P L Y S L V F I F G F V G N M L V I L I  
430 450 470  
CTGATAAAGTCCAAAGGCTGGAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATC  
L I N C Q R L E S M T D I Y L L N L A I  
490 510 530  
TCTGACCTGTTTTCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCAGTGG  
S D L F F L L T V P F W A H Y A A A Q W  
550 570 590  
GACTTTGGAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCT  
D F G N T M C Q L L T G L Y F I G F F S  
610 630 650  
GGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTATCGTCCATGCTGTG  
G I F F I I L L T I D R Y L A I V H A V  
670 690 710  
TTTGCTTTAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTG  
F A L K A R T V T F G V V T S V I T W V  
730 750 770  
GTGGCTGTGTTTGGCTCTCTCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTT  
V A V F A S L P G I I F T R S Q K E G L  
790 810 830  
CATTACACCTGCAGCTCTCATTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAG  
H Y T C S S H F P Y S Q Y Q F W K N F Q  
850 870 890  
ACATTAAAGATAGTCATCTTGGGGCTGGTCTGCCGCTGCTTGTGTCATGGTCATCTGCTAC  
T L K I V I L G L V L P L L V M V I C Y  
910 930 950  
TCGGGAATCCTAAAACTCTGCTTCCGTGTGCAATGAGAAGAAGAGGCACAGGGCTGTG  
S G I L K T L L R C R N E K K R H R A V

FIG.1A

970 990 1010  
AGGCTTATCTTCACCATCATGATTGTTTATTTCTCTTCTGGGCTCCCTACAACATTGTC  
R L I F T I M I V Y F L F W A P Y N I V  
1030 1050 1070  
CTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGG  
L L L N T F Q E F F G L N N C S S S N R  
1090 1110 1130  
TTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCC  
L D Q A M Q V T E T L G M T H C C I N P  
1150 1170 1190  
ATCATCTATGCCTTTGTCTGGGAGAAAGTTTCAGAACTACCTCTTAGTCTTCTTCCAAAAG  
I I Y A F V G E K F R N Y L L V F F Q K  
1210 1230 1250  
CACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGCGA  
H I A K R F C K C C S I F Q Q E A P E R  
1270 1290 1310  
GCAAGCTCAGTTTACACCCGATCCACTGGGAGCAGGAAATATCTGTGGGCTTGTGACAC  
A S S V Y T R S T G E Q E I S V G L \*  
1330 1350 1370  
GGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTTTTTCATACACA  
1390 1410  
GCCTGGGCTGGGGGTGGGGTGAAGAGGTCTTTT

FIG.1B

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4  QVSSPIYDINYYTSEPCPKINVKQIAARLLPPLYSLVFIFGFVGNMLVIL 53
   :  . . . : | . : | . : | | : | | | : | . | | | | | | | | | | : |
18  EEVTTFFDYDY . . GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVL 65

54  ILINCQRLESMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQL 103
   | | | | . : | . : | | | | | | | | | | : | | : | | : | | | . | | | . | |
66  ILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKL 115

104  LTGLYF IGFFSGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITW 153
   : | | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | |
116  FTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITW 165

154  VVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQFWKNFQTLKIVILGL 203
   : | | | | | : | | | | | : : | | : | . | . . | | : | . | : . | | |
166  LVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG . . . WNNFHTIMRNILGL 211

204  VLPLLVMVICYSGILKTLLRCRNEKKRHRÄVRLIFTIMIVYFLFWAPYNI 253
   | | | | : | | | | | | | | | | | | | | | | | | : | | | | | | | . | | |
212  VLPLLIMVICYSGILKTLLRCRNEKKRHRÄVRVIFTIMIVYFLFWTPYNI 261

254  VLLNNTFQEFFGLNNCSSSÄRLDQAMQVTETLGMTHCCINPIIYAFVGEK 303
   | : | | | | | | | | | . | | . | . . | | | | | | | | | | | | | | | |
262  VILLNNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK 311

304  FRNYLLVFFQKHI AKRFCKCCSIFQQEAPÄRASSVYTRS . . . TGEQEISV 350
   | | . . : : . : | | : | . : . . | : . . | | . : . . : : | :
312  FRSLFHIALGCRIA . PLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

351  G 351
   |
361  G 361

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FIG. 2

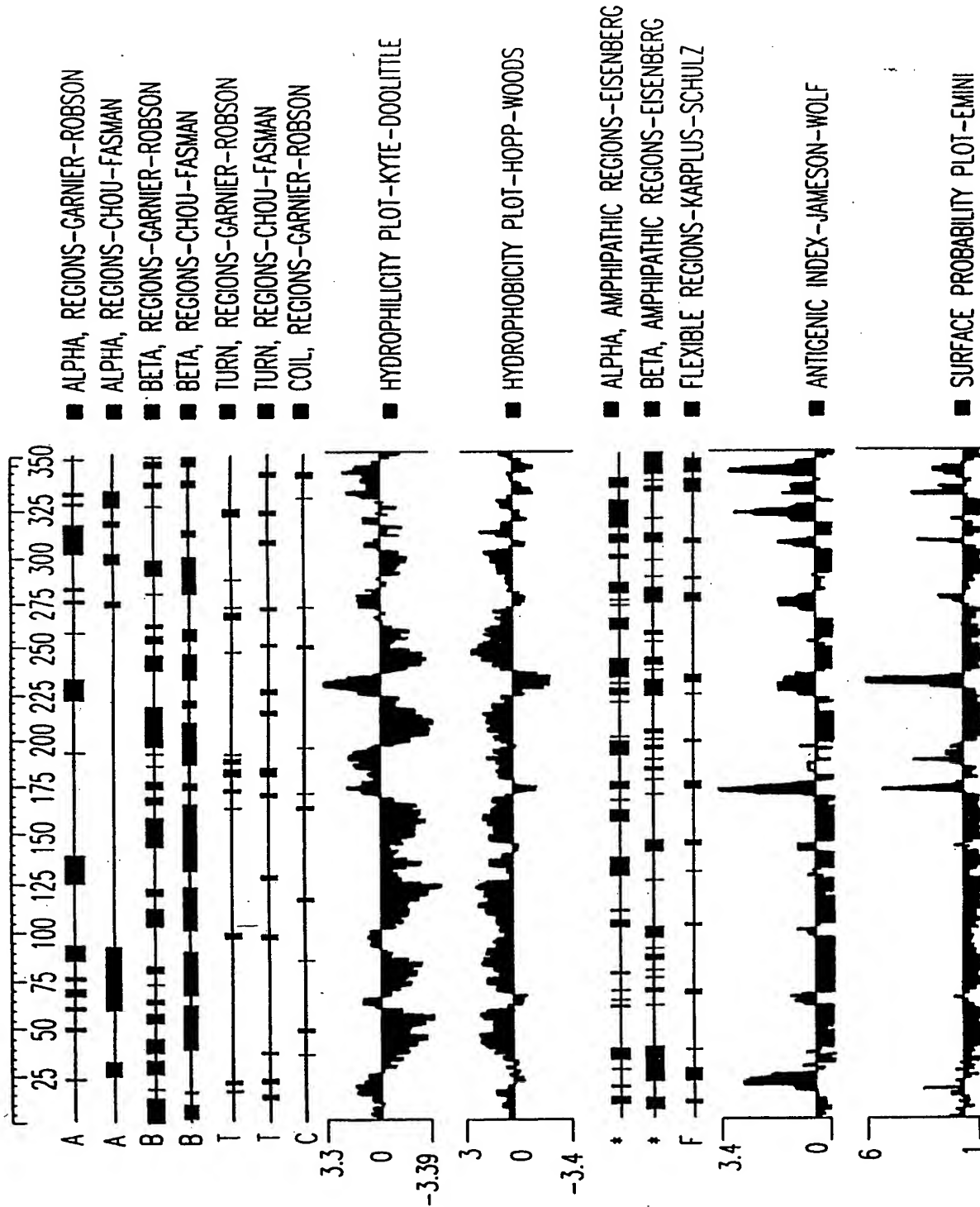


FIG.3

**Anti-CCR5 1D8 VH Sequence**

1 CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC  
 1 Q V Q L Q E S G P G L V K P S E T L S L

**CDR1**

61 ACC TGC ACT GTC TCT GGT GGC TCC ATC AGT AGT TTC TAC TGG AGC TGG ATC CGG CAG CCC  
 21 T C T V S G G S I S S F Y W S W I R Q P

**CDR2**

121 GCC GGG AAG GGA CTG GAC TGG ATT GGG CGT ATC TAT ACC AGC GGG AAC ACC AAC TAC AAC  
 41 A G K G L D W I G R I Y T S G N T N Y N

181 CCC TCC CTC AAG AGT CGA GTC ACC ATG TCA GTA GAC ACG TCC AAG AAC CGG TTC TCC CTG  
 61 P S L K S R V T M S V D T S K N R F S L

241 AAA CTG AGC TCT GTG ACC GCC GCG GAC ACG GCC GTG TAT TAC TGT GCG AGA GAT CGG GCG  
 81 K L S S V T A A D T A V Y Y C A R D R G

**CDR3**

301 AGC AGC TGG TAC CCC GAT GCT TTT GAT ATC TGG GGC CAA GGG ACA ATG GTC ACC GTC TCC  
 101 S S W Y P D A F D I W G Q G T M V T V S

361 TCA

121 S

**Anti-CCR5 1D8 VK Sequence**

1 GAT ATT GTG TTG ACG CAT TCT CCA GGC ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC  
 1 D I V L T H S P G T L S L S P G E R A T

**CDR1**

61 CTC TCC TGC AGG GCC AGT CAG CGT GTT ACC AGC AGC TGC TTA GCC TGG TAC CAG CAG AAA  
 21 L S C R A S Q R V T S S C L A W Y Q Q K

**CDR2**

121 CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GGT ACA TCC AGC AGG GCC ACT GGC ATC CCA  
 41 P G Q A P R L L I Y G T S S R A T G I P

181 GAC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGA CTG GAG  
 61 D R F S G S G S G T D F T L T I S R L E

**CDR3**

241 CCT GAA GAT TTT GCA GTG TAT TAC TGT CAG CAG TAT GTT AGC TCA CCT CTC ACC TTC GGC  
 81 P E D F A V Y Y C Q Q Y V S S P L T F G

301 CAA GGG ACA CGA CTC GAG ATC AAA CGT

101 Q G T R L E I K R

**FIG.4**

**Anti-CCR5 3C9 VH**

1 GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTA AAG TCT GGG GGG TCC CTT AGA CTC 60  
 1 E V Q L V E S G G G L V K S G G S L R L 20

**CDR1**

61 TCC TGT GCA GCC TCC GGA TTC ACT TTC AGT AAC GCC TGG ATG ACC TGG GTC CGC CAG GCT 120  
 21 S C A A S G F T F S N A W M T W V R Q A 40

**CDR2**

121 CCA GGG AAG AGG CTG GAG TGG GTT GGC CGT ATT AAA AGC AAT GCT GAT GGT GGG TCA ACA 180  
 41 P G K R L E W V G R I K S N A D G G S T 60

181 GAC TAC GCT GCA CCC GTG AAA GGC AGA TTC ACC ATC TCA AGA GAT GAT TCA AAA AAC ACG 240  
 61 D Y A A P V K G R F T I S R D D S K N T 80

241 CTG TAT CTG CAA ATG AAC AGC CTG AAA ACC GAG GAC ACA GCC GTG TAT TAC TGT AAC ACA 300  
 81 L Y L Q M N S L K T E D T A V Y Y C N T 100

**CDR3**

301 GAT AAG GGT GGG AGC TAC CCC TAC TAC TAC GGT ATG GAC GTC TGG GGC CAA GGG ACC 360  
 101 D K G G S Y P Y Y Y Y G M D V W G Q G T 120

361 ACG GTC ACC GTC TCC TCA G 379  
 121 T V T V S S 127

**Anti-CCR5 3C9 VK**

1 GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC 60  
 1 D I Q M T Q S P S S L S A S V G D R V T 20

**CDR1**

61 ATC ACT TGC CGG GCA AGT CAG GGC ATT AGA AAT GAT TTA GGC TGG TAT CAG CAG AAA CCA 120  
 21 I T C R A S Q G I R N D L G W Y Q Q K P 40

**CDR2**

121 GGG AAA GCC CCT AAG CGC CTG ATC TAT GAT GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA 180  
 41 G K A P K R L I Y D A S S L Q S G V P S 60

181 AGG TTC AGC GGC AGT GGA TCT GGG ACA GAA TTC ACT CTC ACA ATC AGC AGC GTG CAG CCT 240  
 61 R F S G S G S G T E F T L T I S S L Q P 80

**CDR3**

241 GAA GAT TTT GCA ACT TAT TAC TGT CTA CAG CAT AAT AGT TAC CCA TTC ACT TTC GGC CCT 300  
 81 E D F A T Y Y C L Q H N S Y P F T F G P 100

301 GGG ACC AAA GTG GAT ATC AAA CGA 324  
 101 G T K V D I K R 108

**FIG.5**

**Anti-CCR5 9E6 VH**

1 GAG GTG CAG CTG GTG GAG TCT GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC 60  
 1 E V Q L V E S G P G L V K P S E T L S L 20

**CDR1**

61 ACC TGC ACT GTC TCT GGT GGC TCC ATC AGT AGT TAC TAC TGG AGC TGG ATC CCG CAG CCC 120  
 21 T C T V S G G S I S S Y Y W S W I R Q P 40

**CDR2**

121 CCA GGG AAG GGA CTG GAG TGG ATT GCG TAT ATC TAT TAC AGT GGG AGC ACC AAC TAC AAC 180  
 41 P G K G L E W I G Y I Y Y S G S T N Y N 60

181 CCC TCC CTC AAG AGT CGA GTC ACC ATA TCA GTA GAC ACG TCC AAG AAC CAG TTC TCC CTG 240  
 61 P S L K S R V T I S V D T S K N Q F S L 80

241 AAG CTG AGC TCT GTG ACC GCT GCG GAC ACG GCC GTG TAT TAC TGT GCG AGA GAT GTC ATG 300  
 81 K L S S V T A A D T A V Y Y C A R D V M 100

**CDR3**

301 CAG CAG CCG GTA CGG GGT TAC TAC TAC TAC TAC GGT ATG GAC GTC TGG GGC CAA GGA ACC 360  
 101 Q Q P V R G Y Y Y Y Y G M D V W G Q G T 120

361 CTG GTC ACC GTC TCC TCA 378  
 121 L V T V S S 126

**Anti-CCR5 9E6 VK**

1 GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT TTG TCT CCA GGG GAA AGA GTC ACC 60  
 1 E I V L T Q S P G T L S L S P G E R V T 20

**CDR1**

61 CTC TCC TGC AGG GCC AGT CAG AGA GTT AGC AAC ACC TAC TTA GCC TGG TAC CAG CAG AAA 120  
 21 L S C R A S Q R V S N S Y L A W Y Q Q K 40

**CDR2**

121 CCT GGC CAG GCT CCC AGG TTC CTC ATC TAT GGT GTA TCC AGC AGG GCC ACT GGC ATC CCA 180  
 41 P G Q A P R F L I Y G V S S R A T G I P 60

181 GAC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGA CTG GAG 240  
 61 D R F S G S G S G T D F T L T I S R L E 80

**CDR3**

241 CCT GAA GAT TTT GCA GTG TAT TAC TGT CAG CAG TAT GGT AGT TCA CCG TGG ACG TTC GGC 300  
 81 P E D F A V Y Y C Q Q Y G S S P W T F G 100

301 CAA GGG ACC AAG GTG GAA ATC AAA CGA 327  
 101 Q G T K V E I K R 109

**FIG.6**